OIPE

#3

RAW SEQUENCE LISTING   DATE: 11/13/2001
PATENT APPLICATION: US/09/944,602   TIME: 13:43:06

Input Set : A:\es.txt
Output Set: N:\CRF3\11132001\I944602.raw

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  3 <110> APPLICANT: Pecker, Iris
  4         Vlodavsky, Israel
  5         Friedman , Yael
  6         Perets, Tuvia
  8 <120> TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES AND THEIR USE IN
RESEARCH AND
  9         MEDICAL APPLICATIONS
 11 <130> FILE REFERENCE: 01/22380
W--> 12 <140> CURRENT APPLICATION NUMBER: US 09/944,602 0
 13 <141> CURRENT FILING DATE: 2001-09-04
 15 <150> PRIOR APPLICATION NUMBER: US 09/759,207
 16 <151> PRIOR FILING DATE: 2001-01-16
 18 <150> PRIOR APPLICATION NUMBER: US 09/322,977
 19 <151> PRIOR FILING DATE: 1999-06-01
 21 <150> PRIOR APPLICATION NUMBER: US 09/071,739
 22 <151> PRIOR FILING DATE: 1998-05-01
 24 <150> PRIOR APPLICATION NUMBER: US 08/922,180
 25 <151> PRIOR FILING DATE: 1997-09-02
 27 <160> NUMBER OF SEQ ID NOS: 7
 29 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1721
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1
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 41 cgctgggtcc cctctcccct ggcgccctgc cccgacctgc gcaagcacag gacgtcgtgg    180
 43 acctggactt cttcacccag gagccgctgc acctggtgag cccctcgttc ctgtccgtca    240
 45 ccattgacgc caacctggcc acggacccgc ggttcctcat cctcctgggt tctccaaagc    300
 47 ttcgtacctt ggccagaggc ttgtctcctg cgtacctgag gtttggtggc accaagacag    360
 49 acttcctaat tttcgatccc aagaaggaat caacctttga agagagaagt tactggcaat    420
 51 ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tcctgatgtg gaggagaagt    480
 53 tacggttgga atggccctac caggagcaat tgctactccg agaacactac cagaaaaagt    540
 55 tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct    600
 57 caggactgga cttgatcttt ggcctaaatg cgttattaag aacagcagat ttgcagtgga    660
 59 acagttctaa tgctcagttg ctcctggact actgctcttc caaggggtat aacatttctt    720
 61 gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt    780
 63 cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa    840
 65 atgcaaaact ctatggtcct gatgttggtc agcctcgaag aaagacggct aagatgctga    900
 67 agagcttcct gaaggctggt ggagaagtga ttgattcagt tacatggcat cactactatt    960
 69 tgaatggacg gactgctacc agggaagatt ttctaaaccc tgatgtattg gacatttta    1020
 71 tttcatctgt gcaaaaagtt ttccaggtgg ttgagagcac caggcctggc aagaaggtct    1080
 73 ggttaggaga aacaagctct gcatatggag gcggagcgcc cttgctatcc gacacctttg    1140
 75 cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga atagaagtgg    1200
 77 tgatgaggca agtattcttt ggagcaggaa actaccattt agtggatgaa aacttcgatc    1260
 79 ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aaggtgttaa    1320
 81 tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaca    1380
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83 ctgacaatcc aaggtataaa gaaggagatt taactctgta tgccataaac ctccataacg     1440
85 tcaccaagta cttgcggtta ccctatcctt tttctaacaa gcaagtggat aaataccttc     1500
87 taagaccttt gggacctcat ggattacttt ccaaatctgt ccaactcaat ggtctaactc     1560
89 taaagatggt ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa     1620
91 gttcactggg cttgccagct ttctcatata gttttttttgt gataagaaat gccaaagttg     1680
93 ctgcttgcat ctgaaaataa aatatactag tcctgacact g                        1721
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96 <210> SEQ ID NO: 2
97 <211> LENGTH: 543
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 2

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104 1               5                   10                  15
107 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
108             20              25                  30
111 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
112         35                  40                  45
115 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
116     50                  55                  60
119 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
120 65                  70              75                  80
123 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
124             85                  90                  95
127 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
128             100                 105                 110
131 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
132         115                 120                 125
135 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
136     130                 135                 140
139 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
140 145                 150                 155                 160
143 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
144             165                 170                 175
147 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
148             180                 185                 190
151 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
152         195                 200                 205
155 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
156     210                 215                 220
159 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
160 225                 230                 235                 240
163 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
164             245                 250                 255
167 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
168             260                 265                 270
171 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
172         275                 280                 285
175 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
176     290                 295                 300
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179 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
180 305                 310                 315                 320
183 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
184                 325                 330                 335
187 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
188                 340                 345                 350
191 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
192         355                 360                 365
195 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
196         370                 375                 380
199 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
200 385                 390                 395                 400
203 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
204                 405                 410                 415
207 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
208                 420                 425                 430
211 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
212         435                 440                 445
215 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
216         450                 455                 460
219 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
220 465                 470                 475                 480
223 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
224                 485                 490                 495
227 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
228                 500                 505                 510
231 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
232                 515                 520                 525
235 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
236         530                 535                 540
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 1721
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (63)..(1691)
247 <223> OTHER INFORMATION:
249 <400> SEQUENCE: 3
250 ctagagcttt cgactctccg ctgcgcggca gctggcgggg ggagcagcca ggtgagccca     60
252 ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ccg ctg atg ctg       107
253    Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
254    1               5                  10                  15
256 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga    155
257 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
258                 20                  25                  30
260 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag    203
261 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
262                 35                  40                  45
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W--> 244 (arrow marking line 244)

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Input Set : A:\es.txt
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264 ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc        251
265 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
266         50                  55                  60
268 aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag        299
269 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
270         65                  70                  75
272 ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt        347
273 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
274 80                  85                  90                  95
276 ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc        395
277 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
278                 100                 105                 110
280 ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc        443
281 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
282                 115                 120                 125
284 aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa        491
285 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
286                 130                 135                 140
288 tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag        539
289 Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
290         145                 150                 155
292 ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act        587
293 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
294 160                 165                 170                 175
296 ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta        635
297 Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
298                 180                 185                 190
300 tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc        683
301 Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
302                 195                 200                 205
304 ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc        731
305 Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
306         210                 215                 220
308 aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg        779
309 Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
310         225                 230                 235
312 tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag        827
313 Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys
314 240                 245                 250                 255
316 tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct        875
317 Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro
318         260                 265                 270
320 cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga        923
321 Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly
322         275                 280                 285
324 gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg        971
325 Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg
326         290                 295                 300
328 act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt       1019
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329 Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe
330     305                 310                 315
332 att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct     1067
333 Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro
334 320                 325                 330                 335
336 ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga     1115
337 Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly
338                 340                 345                 350
340 gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat     1163
341 Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp
342             355             '   360                 365
344 aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa     1211
345 Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln
346             370                 375                 380
348 gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat     1259
349 Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp  .
350     385                 390                 395
352 cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc     1307
353 Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly
354 400                 405                 410                 415
356 acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt     1355
357 Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu
358             420                 425                 430
360 cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa     1403
361 Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu
362             435                 440                 445
364 gga gat tta act ctg tat gcc ata aac ctc cat aac gtc acc aag tac     1451
365 Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr
366             450                 455                 460
368 ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt     1499
369 Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu
370     465                 470                 475
372 cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc     1547
373 Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu
374 480                 485                 490                 495
376 aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta     1595
377 Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu
378             500                 505                 510
380 atg gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc     1643
381 Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe
382             515                 520                 525
384 tca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc     1691
385 Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
386             530                 535                 540
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392 <210> SEQ ID NO: 4
393 <211> LENGTH: 26
394 <212> TYPE: DNA
395 <213> ORGANISM: Artificial sequence
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VERIFICATION SUMMARY   DATE: 11/13/2001
PATENT APPLICATION: **US/09/944,602**   TIME: 13:43:07

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11132001\I944602.raw**

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L:244 M:283 W: Missing Blank Line separator, <220> field identifier